

[Sequence Sheet 1]

Sequence No.: 1

Length of sequence: 582

Type of sequence: Amino acid

Topology: Linear

Class of sequence: Protein

Sequence

Met Ser Pro Ala Pro Arg Pro Ser Arg Cys Leu Leu Leu Pro Leu
1 5 10 15
Leu Thr Leu Gly Thr Ala Leu Ala Ser Leu Gly Ser Ala Gln Ser
20 25 30
Ser Ser Phe Ser Pro Glu Ala Trp Leu Gln Gln Tyr Gly Tyr Leu
35 40 45
Pro Pro Gly Asp Leu Arg Thr His Thr Gln Arg Ser Pro Gln Ser
50 55 60
Leu Ser Ala Ala Ile Ala Ala Met Gln Lys Phe Tyr Gly Leu Gln
65 70 75
Val Thr Gly Lys Ala Asp Ala Asp Thr Met Lys Ala Met Arg Arg
80 85 90
Pro Arg Cys Gly Val Pro Asp Lys Phe Gly Ala Glu Ile Lys Ala
95 100 105
Asn Val Arg Arg Lys Arg Tyr Ala Ile Gln Gly Leu Lys Trp Gln
110 115 120
His Asn Glu Ile Thr Phe Cys Ile Gln Asn Tyr Thr Pro Lys Val
125 130 135
Gly Glu Tyr Ala Thr Tyr Glu Ala Ile Arg Lys Ala Phe Arg Val
140 145 150
Trp Glu Ser Ala Thr Pro Leu Arg Phe Arg Glu Val Pro Tyr Ala
155 160 165

[Sequence Sheet 2]

Sequence No.: 1 (continued)

Tyr Ile Arg Glu Gly His Glu Lys Gln Ala Asp Ile Met Ile Phe	170	175	180
Phe Ala Glu Gly Phe His Gly Asp Ser Thr Pro Phe Asp Gly Glu	185	190	195
Gly Gly Phe Leu Ala His Ala Tyr Phe Pro Gly Pro Asn Ile Gly	200	205	210
Gly Asp Thr His Phe Asp Ser Ala Glu Pro Trp Thr Val Arg Asn	215	220	225
Glu Asp Leu Asn Gly Asn Asp Ile Phe Leu Val Ala Val His Glu	230	235	240
Leu Gly His Ala Leu Gly Leu Glu His Ser Ser Asp Pro Ser Ala	245	250	255
Ile Met Ala Pro Phe Tyr Gln Trp Met Asp Thr Glu Asn Phe Val	260	265	270
Leu Pro Asp Asp Asp Arg Arg Gly Ile Gln Gln Leu Tyr Gly Gly	275	280	285
Glu Ser Gly Phe Pro Thr Lys Met Pro Pro Gln Pro Arg Thr Thr	290	295	300
Ser Arg Pro Ser Val Pro Asp Lys Pro Lys Asn Pro Thr Tyr Gly	305	310	315
Pro Asn Ile Cys Asp Gly Asn Phe Asp Thr Val Ala Met Leu Arg	320	325	330
Gly Glu Met Phe Val Phe Lys Lys Arg Trp Phe Trp Arg Val Arg	335	340	345
Asn Asn Gln Val Met Asp Gly Tyr Pro Met Pro Ile Gly Gln Phe	350	355	360
Trp Arg Gly Leu Pro Ala Ser Ile Asn Thr Ala Tyr Glu Arg Lys	365	370	375

[Sequence Sheet 3]

Sequence No.: 1 (continued)

Asp Gly Lys Phe Val Phe Phe Lys Gly Asp Lys His Trp Val Phe	380	385	390
Asp Glu Ala Ser Leu Glu Pro Gly Tyr Pro Lys His Ile Lys Glu	395	400	405
Leu Gly Arg Gly Leu Pro Thr Asp Lys Ile Asp Ala Ala Leu Phe	410	415	420
Trp Met Pro Asn Gly Lys Thr Tyr Phe Phe Arg Gly Asn Lys Tyr	425	430	435
Tyr Arg Phe Asn Glu Glu Leu Arg Ala Val Asp Ser Glu Tyr Pro	440	445	450
Lys Asn Ile Lys Val Trp Glu Gly Ile Pro Glu Ser Pro Arg Gly	455	460	465
Ser Phe Met Gly Ser Asp Glu Val Phe Thr Tyr Phe Tyr Lys Gly	470	475	480
Asn Lys Tyr Trp Lys Phe Asn Asn Gln Lys Leu Lys Val Glu Pro	485	490	495
Gly Tyr Pro Lys Ser Ala Leu Arg Asp Trp Met Gly Cys Pro Ser	500	505	510
Gly Gly Arg Pro Asp Glu Gly Thr Glu Glu Glu Thr Glu Val Ile	515	520	525
Ile Ile Glu Val Asp Glu Glu Gly Gly Gly Ala Val Ser Ala Ala	530	535	540
Ala Val Val Leu Pro Val Leu Leu Leu Leu Leu Val Leu Ala Val	545	550	555
Gly Leu Ala Val Phe Phe Phe Arg Arg His Gly Thr Pro Arg Arg	560	565	570
Leu Leu Tyr Cys Gln Arg Ser Leu Leu Asp Lys Val	575	580	

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[Sequence Sheet 5]

Sequence No.: 2 (continued)

AGTTCAGTGCCTACC GAAGACAAAGGCGCC CCGAGGGAGTGGCGG TCCGACCCCAGGGCG 60

TGGGCCCCGGCCGGG AGCCACACTGCCCCG CTGACCCGGTGGTCT CGGACCATGTCTCCC 120
MetSerPro
/

GCCCCAAGACCCTCC CGTTGTCTCTGCTC CCCCTGCTCAGGCTC GGCACCGCGCTCGCC 180
AlaProArgProSer ArgCysLeuLeuLeu ProLeuLeuThrLeu GlyThrAlaLeuAla
5 10 15 20

TCCCTCGGCTCGGCC CAAAGCAGCAGCTTC AGCCCCGAAGCCTGG CTACAGCAATATGGC 240
SerLeuGlySerAla GlnSerSerSerPhe SerProGluAlaTrp LeuGlnGlnTyrGly
25 30 35 40

TACCTGCCTCCCGGG GACCTACGTACCCAC ACACAGCGCTCACCC CAGTCACTCTCAGCG 300
TyrLeuProProGly AspLeuArgThrHis ThrGlnArgSerPro GlnSerLeuSerAla
45 50 55 60

GCCATCGCTGCCATG CAGAAGTTTACGGC TTGCAAGTAACAGGC AAAGCTGATGCAGAC 360
AlaIleAlaAlaMet GlnLysPheTyrGly LeuGlnValThrGly LysAlaAspAlaAsp
65 70 75 80

ACCATGAAGGCCATG AGGCGCCCCCGATGT GGTGTTCCAGACAAG TTTGGGGCTGAGATC 420
ThrMetLysAlaMet ArgArgProArgCys GlyValProAspLys PheGlyAlaGluIle
85 90 95 100

AAGGCCAATGTTCGA AGGAAGCGCTACGCC ATCCAGGGTCTCAAA TGGCAACATAATGAA 480
LysAlaAsnValArg ArgLysArgTyrAla IleGlnGlyLeuLys TrpGlnHisAsnGlu
105 110 115 120

ATTACTTTCTGCATC CAGAATTACACCCCC AAGTGGGCGAGTAT GCCACATACGAGGCC 540
IleThrPheCysIle GlnAsnTyrThrPro LysValGlyGluTyr AlaThrTyrGluAla
125 130 135 140

ATTCGCAAGGCGTTC CGCGTGTGGGAGAGT GCCACACCACTGCGC TTCCGCGAGGTGCCC 600
IleArgLysAlaPhe ArgValTrpGluSer AlaThrProLeuArg PheArgGluValPro
145 150 155 160

TATGCCTACATCCGT GAGGGCCATGAGAAG CAGGCCGACATCATG ATCTTCTTTGCCGAG 660
TyrAlaTyrIleArg GluGlyHisGluLys GlnAlaAspIleMet IlePhePheAlaGlu
165 170 175 180

[Sequence Sheet 6]

Sequence No.: 2 (continued)

GGCTTCCATGGCGAC	AGCACGCCCTTCGAT	GGTGAGGGCGGCTTC	CTGGCCCATGCCTAC	720
GlyPheHisGlyAsp 185	SerThrProPheAsp 190	GlyGluGlyGlyPhe 195	LeuAlaHisAlaTyr 200	
TTCCCAGGGCCCAAC	ATTGGAGGAGACACC	CACTTTGACTCTGCC	GAGCCTTGGACTGTC	780
PheProGlyProAsn 205	IleGlyGlyAspThr 210	HisPheAspSerAla 215	GluProTrpThrVal 220	
AGGAATGAGGATCTG	AATGGAAATGACATC	TTCCTGGTGGCTGTG	CACGAGCTGGGCCAT	840
ArgAsnGluAspLeu 225	AsnGlyAsnAspIle 230	PheLeuValAlaVal 235	HisGluLeuGlyHis 240	
GCCCTGGGGCTCGAG	CATTCCAGTGACCCC	TCGGCCATCATGGCA	CCCTTTTACCAGTGG	900
AlaLeuGlyLeuGlu 245	HisSerSerAspPro 250	SerAlaIleMetAla 255	ProPheTyrGlnTrp 260	
ATGGACACGGAGAAT	TTGTGCTTCCCGAT	GATGACCGCCGGGGC	ATCCAGCAACTTTAT	960
MetAspThrGluAsn 265	PheValLeuProAsp 270	AspAspArgArgGly 275	IleGlnGlnLeuTyr 280	
GGGGGTGAGTCAGGG	TTCCCACCAAGATG	CCCCCTCAACCCAGG	ACTACCTCCCGGCCT	1020
GlyGlyGluSerGly 285	PheProThrLysMet 290	ProProGlnProArg 295	ThrThrSerArgPro 300	
TCTGTTCTTGATAAA	CCCCAAAACCCACC	TATGGGCCCAACATC	TGTGACGGGAACTTT	1080
SerValProAspLys 305	ProLysAsnProThr 310	TyrGlyProAsnIle 315	CysAspGlyAsnPhe 320	
GACACCGTGGCCATG	CTCCGAGGGGAGATG	TTTGTCTTCAAGAAG	CGCTGGTTCTGGCGG	1140
AspThrValAlaMet 325	LeuArgGlyGluMet 330	PheValPheLysLys 335	ArgTrpPheTrpArg 340	
GTGAGGAATAACCAA	GTGATGGATGGATAC	CCAATGCCATTGGC	CAGTTCTGGCGGGGC	1200
ValArgAsnAsnGln 345	ValMetAspGlyTyr 350	ProMetProIleGly 355	GlnPheTrpArgGly 360	
CTGCCTGCGTCCATC	AACACTGCCTACGAG	AGGAAGGATGGCAAA	TTCGTCTTCTTCAAA	1260
LeuProAlaSerIle 365	AsnThrAlaTyrGlu 370	ArgLysAspGlyLys 375	PheValPhePheLys 380	
GGAGACAAGCATTGG	GTGTTTCATGAGGCG	TCCCTGGAACCTGGC	TACCCCAAGCACATT	1320
GlyAspLysHisTrp 385	ValPheAspGluAla 390	SerLeuGluProGly 395	TyrProLysHisIle 400	

[Sequence Sheet 7]

Sequence No.: 2 (continued)

AAGGAGCTGGCCCGA	GGGCTGCCTACCGAC	AAGATTGATGCTGCT	CTCTTCTGGATGCCC	1380
LysGluLeuGlyArg	GlyLeuProThrAsp	LysIleAspAlaAla	LeuPheTrpMetPro	
405	410	415	420	
AATGGAAGACCTAC	TTCTTCGGTGGAAAC	AAGTACTACCGTTTC	AACGAAGAGCTCAGG	1440
AsnGlyLysThrTyr	PhePheArgGlyAsn	LysTyrTyrArgPhe	AsnGluGluLeuArg	
425	430	435	440	
GCAGTGGATAGCGAG	TACCCCAAGAACATC	AAAGTCTGGGAAGGG	ATCCCTGAGTCTCCC	1500
AlaValAspSerGlu	TyrProLysAsnIle	LysValTrpGluGly	IleProGluSerPro	
445	450	455	460	
AGAGGGTCATTCATG	GGCAGCGATGAAGTC	TTCACCTACTTCTAC	AAGGGGAACAAATAC	1560
ArgGlySerPheMet	GlySerAspGluVal	PheThrTyrPheTyr	LysGlyAsnLysTyr	
465	470	475	480	
TGGAATTCACAAC	CAGAAGCTGAAGCTA	GAACCGGGCTACCCC	AAGTCAGCCCTGAGG	1620
TrpLysPheAsnAsn	GlnLysLeuLysVal	GluProGlyTyrPro	LysSerAlaLeuArg	
485	490	495	500	
GACTGGATGGGCTGC	CCATCGGGAGGCCGG	CCGGATGAGGGGACT	GAGGAGGAGACGGAG	1680
AspTrpMetGlyCys	ProSerGlyGlyArg	ProAspGluGlyThr	GluGluGluThrGlu	
505	510	515	520	
GTGATCATCATTGAG	GTGGACGAGGAGGGC	GCGGGGCGGTGAGC	GCGGCTGCCGTGGTG	1740
ValIleIleIleGlu	ValAspGluGluGly	GlyGlyAlaValSer	AlaAlaAlaValVal	
525	530	535	540	
CTGCCCCGTGCTGCTG	CTGCTCCTGGTGCTG	GCGGTGGGCCTTGCA	GTCTTCTTCTCAGA	1800
LeuProValLeuLeu	LeuLeuLeuValLeu	AlaValGlyLeuAla	ValPhePhePheArg	
545	550	555	560	
CGCCATGGGACCCCC	AGGCGACTGCTCTAC	TGCCAGCGTTCCTG	CTGGACAAGGTCTGA	1860
ArgHisGlyThrPro	ArgArgLeuLeuTyr	CysGlnArgSerLeu	LeuAspLysVal...	
565	570	575	580	
CGCCCATCCGCCGGC	CGCCCCACTCCTACC	ACAAGGACTTTGCCT	CTGAAGGCCAGTGGC	1920
AGCAGGTGGTGCTGG	GTGGGCTGCTCCCAT	CGTCCCGAGCCCCCT	CCCCGCAGCCTCCTT	1980

[Sequence Sheet 8]

Sequence No.: 2 (continued)

GCTTCTCTCTGTCCC CTGGCTGGCCTCCTT CACCCTGACCGCCTC CCTCCCTCCTGCCCC 2040
GGCATTGCATCTTCC CTAGATAGGTCCCCT GAGGGCTGAGTGGGA GGGCGGCCCTTTCCA 2100
GCCTCTGCCCCCTCAG GGAACCCCTGTAGCT TTGTGTCTGTCCAGC CCCATCTGAATGTGT 2160
TGGGGGCTCTGCACT TGAAGGCAGGACCCT CAGACCTCGCTGGTA AAGGTCAAATGGGGT 2220
CATCTGCTCCTTTTC CATCCCCTGACATAC CTTAACCTCTGAACT CTGACCTCAGGAGGC 2280
TCTGGGGAACCTCCAG GCCTGAAAGCCCCAG GTGTACCCAATTGGC AGCCTCTCACTACTC 2340
TTTCTGGCTAAAAGG AATCTAATCTTGTG AGGGTAGAGACCCTG AGACAGTGTGAGGGG 2400
GTGGGGACTGCCAAG CCACCCTAAGACCTT GCGAGGAAAACCTCAG AGAGGCTCTTCCTTG 2460
CTCAGTCAGTCAAGT TCCTCGGAGATCTT CTCTGCCTCACCTAC CCCAGGGAACCTCCA 2520
AGGAAGGAGCCTGAG CCACTGGGGACTAAG TGGGCAGAAAGAAACC CTTGGCAGCCCTGTG 2580
CCTCTCGAATGTTAG CCTTGGATGGGGCTT TCACAGTTAGAAGAG CTGAAACCAGGGGTG 2640

[Sequence Sheet 9]

Sequence No.: 2 (continued)

CAGCTGTCAGCTAGG GTGGGCGCGGTGGGA GAGGCGCGGGTCAGA GCCCTGGGGGTGAGC 2700

CTTAAGGCCACAGAG AAAGAACCTTGCCCA AACTCAGGCAGCTGG GGCTGAGGCCCAAAG 2760

GCAGAACAGCCAGAG GGGGCAAGGAGGGGAC CAAAAAGGAAATGA GGACGTGCAGCAGCA 2820

TTGGAAGGCTGGGGC CCGGCAGCCAGGTTA AAGCTAACAGGGGGC CATCAGGGTGGGCTT 2880

GTGGAGCTCTCAGGA AGGGCCCTGAGGAAG GCACACTTGCTCCTG TTGGTCCCTGTCTT 2940

GCTGCCCAGGCAGGG TGGAGGGGAAGGTA GGGCAGCCAGAGAAA GGAGCAGAGAAGGCA 3000

CACAAACGAGGAATG AGGGGCTTCACGAGA GGCCACAGGGCCTGG CTGGCCACGCTGTCC 3060

CGGCCTGCTACCAT CTCAGTGAGGGACAG GAGCTGGGGCTGCTT AGGCTGGGTCCACGC 3120

TTCCCTGGTGCCAGC ACCCTCAAGCCTGT CTCACCAGTGGCCTG CCCTCTCGCTCCCC 3180

ACCCAGCCCACCCAT TGAAGTCTCCTTGGG TCCAAAGGTGGGCA TGGTACCGGGGACTT 3240

GGGAGAGTGAGACCC AGTGGAGGGAGCAAG AGGAGAGGGATGTGG GGGGGTGGGGCACGG 3300

GTAGCGGAAATCGCG TGAACGGTGCTGGCA GTTCGGCTAGATTTC TGTCTTGTGTTTTT 3360

TTTGTGTTGTTTAAAT GTATATGTTTATTAT AATATTATATAT

[Sequence Sheet 10]

Sequence No.: 3

Length of sequence: 7

Type of sequence: Amino acid

Topology: Linear

Class of sequence: Peptide

Fragment type: Intermediate fragment

Sequence

Pro	Arg	Cys	Gly	Val	Pro	Asp
1				5		

[Sequence Sheet 11]

Sequence No.: 4

Length of sequence: 9

Type of sequence: Amino acid

Topology: Linear

Class of sequence: Peptide

Fragment type: Intermediate fragment

Sequence

Gly	Asp	Ala	His	Phe	Asp	Asp	Asp	Glu
1				5				

[Sequence Sheet 12]

Sequence No.: 5

Length of sequence: 20

Type of sequence: Nucleic acid

Number of chain: Double strand

Topology: Linear

Class of sequence: Other nucleic acid, synthetic DNA

Sequence

CC (C/A) (C/A) G (G/A/C) TG (T/C) (C/G) G (G/A/C) (G/A) (A/T) (G/C/T) CC
(T/A) GA

[Sequence Sheet 13]

Sequence No.: 6

Length of sequence: 25

Type of sequence: Nucleic acid

Number of chain: Double strand

Topology: Linear

Class of sequence: Other nucleic acid, synthetic DNA

Sequence

(T/C) TC (G/A) T (G/C) (G/A/C) TC (G/A) TC (G/A) AA (G/A) TG (G/A) (G/A)
(C/A/T) (G/A) TC (T/C)

[Sequence Sheet 14]

Sequence No.: 7

Length of sequence: 27

Type of sequence: Amino acid

Topology: Linear

Class of sequence: Peptide

Fragment type: Intermediate fragment

Sequence

Gly	Gly	Gly	Ala	Val	Ser	Ala	Ala	Ala	Val
1				5					10
Val	Leu	Pro	Val	Leu	Leu	Leu	Leu	Leu	Val
				15					20
Leu	Ala	Val	Gly	Leu	Ala	Val	Phe	Phe	Phe
				25					

[Sequence Sheet 15]

Sequence No.: 8

Length of sequence: 14

Type of sequence: Amino acid

Topology: Linear

Class of sequence: Peptide

Sequence

Arg	Glu	Val	Pro	Tyr	Ala	Tyr	Ile	Arg	Glu
1				5					10

Gly His Glu Lys

[Sequence Sheet 16]

Sequence No.: 9

Length of sequence: 14

Type of sequence: Amino acid

Topology: Linear

Class of sequence: Peptide

Sequence

Asp	Gly	Asn	Phe	Asp	Thr	Val	Ala	Met	Leu
1				5					10

Arg	Gly	Glu	Met
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[Sequence Sheet 17]

Sequence No.: 10

Length of sequence: 15

Type of sequence: Amino acid

Topology: Linear

Class of sequence: Peptide

Sequence

Pro	Lys	Ser	Ala	Leu	Arg	Asp	Trp	Met	Gly
1				5					10

Cys	Pro	Ser	Gly	Gly
				15